OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/084,700

DATE: 03/19/2002
TIME: 14:38:45

Input Set : A:\438d1.app
Output Set: N:\CRF3\03192002\J084700.raw

<110> APPLICANT: Seeley, Todd
<120> TITLE OF INVENTION: huBUB3 GENE INVOLVED IN HUMAN CANCERS
<130> FILE REFERENCE: PP-01406.004/200130.438D1
C--> 11 **<140> CURRENT APPLICATION NUMBER: US/10/084,700**
<141> CURRENT FILING DATE: 2002-02-27
<160> NUMBER OF SEQ ID NOS: 32
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 2619
<212> TYPE: DNA
<213> ORGANISM: Homo sapien
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57 gaatgagatt catttcaatg taatgcacta aagcagaaca cgaacttagc ttggcctatt 2040
58 ctaggtagtt ccaaatagta tttttgttgt caaactttaa aatttatatt aatttgcaaa 2100
59 tgtatgtctc tgagtaggac ttggaccttt cctgagattt attttatccg tgatgtattt 2160
60 tttttaattc ttttgataca gagaagggtc ttttttttt taagtatttc agtgaaaact 2220
61 tggtgtaagt ctgaacccat cttttgaaat gtattttctt cattgcaggt ccacctaatc 2280
62 atcctgtgaa agtggtttct ctatggaaag ctttgtttgc ttcctacaaa tacatgctta 2340
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78 20 25 30
79 Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
80 35 40 45
81 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
82 50 55 60
83 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
84 65 70 75 80
85 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
86 85 90 95
87 Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Glu Val Asn Val Met Val
88 100 105 110
89 Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp Pro Arg Thr Pro
90 115 120 125
91 Cys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val Tyr Thr Leu Ser
92 130 135 140
93 Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly Arg Arg Val Leu
94 145 150 155 160
95 Val Trp Asp Leu Arg Asn Met Gly Tyr Val Gln Gln Arg Arg Glu Ser
96 165 170 175
97 Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe Pro Asn Lys Gln
98 180 185 190
99 Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala Val Glu Tyr Leu
100 195 200 205
101 Asp Pro Ser Pro Glu Val Gln Lys Lys Lys Tyr Ala Phe Lys Cys His
102 210 215 220
103 Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro Val Asn Ala Ile
104 225 230 235 240
105 Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly Gly Ser Asp Gly

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107 Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg Leu Cys Gln Phe
108             260                 265                 270
109 His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe Ser Asn Asp Gly
110         275                 280                 285
111 Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu Met Asp Asp Thr
112     290                 295                 300
113 Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val Thr Asp Ala Glu
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115 Thr Lys Pro Lys Ser Pro Cys Thr
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126 gatacataca gtgggtagaa gagaattttc ctgagaataa agaatacttg ataactttac     180
127 tagaacattt aatgaaggaa tttttagata agaagaaata ccacaatgac ccaagattca     240
128 tcagttattg tttaaaattt gctgagtaca acagtgacct ccatcaattt tttgagtttc     300
129 tgtacaacca tgggattgga accctgtcat ccctctgta cattgcctgg gcggggcatc     360
130 tggaagccca aggagagctg cagcatgcca gtgctgtcct tcagagagga attcaaaacc     420
131 aggctgaacc cagagagttc ctgcaacaac aatacaggtt atttcagaca cgcctcactg     480
132 aaacccattt gccagctcaa gctagaacct cagaacctct gcataatgtt caggttttaa     540
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134 agggttcaga gctttctgga gtgatatctt cagcttgtga taaagagtca aatatggaac     660
135 gaagagtgat cacgatttct aaatcagaat attctgtgca ctcatctttg gcatccaaag     720
136 ttgatgttga gcaggttgtt atgtattgca aggagaagct tattcgtggg gaatcagaat     780
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140 aggatctgcc cgcttcccag gaaaggtccg aggttaatcc agcacgtatg gggccaagtg    1020
141 taggctccca gcaggaactg agagcgccat gtcttccagt aacctatcag cagacaccag    1080
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145 ataagagtac tcatgaattc aagccacaga gtggagcaga gatcaaagaa gggtgtgaaa    1320
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154 ccctggcacc cagtcctaag agcccaggag acttcacatc tgctgcacaa cttgcgtcta    1860
155 caccattcca caagcttcca gtggagtcag tgcacatttt agaagataaa gaaaatgtgg    1920
156 tagcaaaaca gtgtacccag gcgactttgg attcttgtga ggaaaacatg gtggtgcctt    1980
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163 gtaaacttcc agccatcaag cccaagactg aatttcaatt gggttctaag ctggtctatg 2400
164 tccatcacct tcttggagaa ggagcctttg cccaggtgta cgaagctacc cagggagatc 2460
165 tgaatgatgc taaaaataaa cagaaatttg ttttaaaggt ccaaaagcct gccaacccct 2520
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167 ttatgaagtt ctattctgcc cacttattcc agaatggcag tgtattagta ggagagctct 2640
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178 tacgtaatag gctaattgta ctgctcttag aatgtaagcg ttcacgaaaa taaaatttgg 3300
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193 Trp Val Glu Glu Asn Phe Pro Glu Asn Lys Glu Tyr Leu Ile Thr Leu
194 35 40 45
195 Leu Glu His Leu Met Lys Glu Phe Leu Asp Lys Lys Lys Tyr His Asn
196 50 55 60
197 Asp Pro Arg Phe Ile Ser Tyr Cys Leu Lys Phe Ala Glu Tyr Asn Ser
198 65 70 75 80
199 Asp Leu His Gln Phe Phe Glu Phe Leu Tyr Asn His Gly Ile Gly Thr
200 85 90 95
201 Leu Ser Ser Pro Leu Tyr Ile Ala Trp Ala Gly His Leu Glu Ala Gln
202 100 105 110
203 Gly Glu Leu Gln His Ala Ser Ala Val Leu Gln Arg Gly Ile Gln Asn
204 115 120 125
205 Gln Ala Glu Pro Arg Glu Phe Leu Gln Gln Gln Tyr Arg Leu Phe Gln
206 130 135 140
207 Thr Arg Leu Thr Glu Thr His Leu Pro Ala Gln Ala Arg Thr Ser Glu

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210                 165                 170                 175
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212             180                 185                 190
213 Leu Ser Gly Val Ile Ser Ser Ala Cys Asp Lys Glu Ser Asn Met Glu
214         195                 200                 205
215 Arg Arg Val Ile Thr Ile Ser Lys Ser Glu Tyr Ser Val His Ser Ser
216     210                 215                 220
217 Leu Ala Ser Lys Val Asp Val Glu Gln Val Val Met Tyr Cys Lys Glu
218 225                 230                 235                 240
219 Lys Leu Ile Arg Gly Glu Ser Glu Phe Ser Phe Glu Glu Leu Arg Ala
220                 245                 250                 255
221 Gln Lys Tyr Asn Gln Arg Arg Lys His Glu Gln Trp Val Asn Glu Asp
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224         275                 280                 285
225 Leu Lys Gln Lys Met Asp Glu Leu His Lys Lys Leu His Gln Val Val
226     290                 295                 300
227 Glu Thr Ser His Glu Asp Leu Pro Ala Ser Gln Glu Arg Ser Glu Val
228 305                 310                 315                 320
229 Asn Pro Ala Arg Met Gly Pro Ser Val Gly Ser Gln Gln Glu Leu Arg
230                 325                 330                 335
231 Ala Pro Cys Leu Pro Val Thr Tyr Gln Gln Thr Pro Val Asn Met Glu
232             340                 345                 350
233 Lys Asn Pro Arg Glu Ala Pro Pro Val Val Pro Pro Leu Ala Asn Ala
234         355                 360                 365
235 Ile Ser Ala Ala Leu Val Ser Pro Ala Thr Ser Gln Ser Ile Ala Pro
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237 Pro Val Pro Leu Lys Ala Gln Thr Val Thr Asp Ser Met Phe Ala Val
238 385                 390                 395                 400
239 Ala Ser Lys Asp Ala Gly Cys Val Asn Lys Ser Thr His Glu Phe Lys
240                 405                 410                 415
241 Pro Gln Ser Gly Ala Glu Ile Lys Glu Gly Cys Glu Thr His Lys Val
242             420                 425                 430
243 Ala Asn Thr Ser Ser Phe His Thr Thr Pro Asn Thr Ser Leu Gly Met
244         435                 440                 445
245 Val Gln Ala Thr Pro Ser Lys Val Gln Pro Ser Pro Thr Val His Thr
246     450                 455                 460
247 Lys Glu Ala Leu Gly Phe Ile Met Asn Met Phe Gln Ala Pro Thr Leu
248 465                 470                 475                 480
249 Pro Asp Ile Ser Asp Asp Lys Asp Glu Trp Gln Ser Leu Asp Gln Asn
250                 485                 490                 495
251 Glu Asp Ala Phe Glu Ala Gln Phe Gln Lys Asn Val Arg Ser Ser Gly
252             500                 505                 510
253 Ala Trp Gly Val Asn Lys Ile Ile Ser Ser Leu Ser Ser Ala Phe His
254         515                 520                 525
255 Val Phe Glu Asp Gly Asn Lys Glu Asn Tyr Gly Leu Pro Gln Pro Lys
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L:11 M:270 C: Current Application Number differs, Wrong Format